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## TECH CENTER 1600/2900



1646

RAW SEQUENCE LISTING DATE: 02/21/2002 PATENT APPLICATION: US/09/825,751A TIME: 11:30:33

Input Set : A:\Cura-251.app

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Output Set: N:\CRF3\02212002\I825751A.raw

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3 <110> APPLICANT: CuraGen Corporation
             Vernet, Corine A.M.
      5
              Fernandes, Elma R
             Taupier, Raymond J
      6
                                                                     ENTERED
      7
             Quinn, Kerry E
      8
              Spytek, Kimberly A
     9
             Rastelli, Luca
             Herrman, John L
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     14 <130> FILE REFERENCE: 15966-750
     16 <140> CURRENT APPLICATION NUMBER: 09/825,751A
C--> 17 <141> CURRENT FILING DATE: 2001-04-30
     19 <150> PRIOR APPLICATION NUMBER: 60/194,314
     20 <151> PRIOR FILING DATE: 2000-04-03
     22 <150> PRIOR APPLICATION NUMBER: 60/225,693
     23 <151> PRIOR FILING DATE: 2000-08-16
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                                      Gln Lys Pro Cys Leu Gln Arg Leu Pro
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     47
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     50 Ser Ala Asp Val Asn Glu Cys Ala Glu Asn Pro Gly Val Cys Thr Asn
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     54 Gly Val Cys Val Asn Thr Asp Gly Ser Phe Arg Cys Glu Cys Pro Phe
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     57 ggc tac agc ctg gac ttc act ggc atc aac tgt gtg gac aca gac gag
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62 Cys Ser Val Gly His Pro Cys Gly Gln Gly Thr Cys Thr Asn Val Ile

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Input Set : A:\Cura-251.app
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67	-	75					80					85					
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70	Met	Thr	Cys	Glu	Asp	Ile	Asp	Glu	Cys	Ser	Leu	Asn	Pro	Leu	Leu	Cys	
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74	Ala	Phe	Arg	Cys	His	Asn	Thr	Glu	Gly	Ser	Tyr	Leu	Cys	Thr	Cys	Pro	
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86	Lys	Asn	Leu	Ile	Gly	Thr	Phe	Ala	Cys	Val	Cys	Pro	Pro	Gly	Met	Arg	
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99 10: 10: 10:	l aco 2 Thi	Phe gaç Glu	Arg g tgo l Cys 220	Cys 205 c cac s His	Asp gac Asp	Cys ato Ile	Asp cgg Arg	Glu cag Gln 225	Gly 210 ggg Gly	Phe ccc Pro	Gln tgo Cys	Pro ttt Phe	Ser gcc Ala 230	Pro 215 gag Glu	Thr g gto l Va	Leu g ctg L Leu	906
99 103 103 103	l aco 2 Thi 3 5 cag	Phe gag Glu gac	Arg g tgo l Cys 220 c ato	Cys 205 c cac His	Asp gac Asp cgg	Cys ato Ile	Asp cgg Arg	Glu cag Gln 225	Gly 210 ggg Gly Gly	Phe ccc Pro	Gln tgc Cys	Pro ttt Phe	Ser gcc Ala 230 gct	Pro 215 gag Glu	Thr gto Val	Leu g ctg L Leu c agg	
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99 10: 10: 10: 10: 10: 10:	l acc 2 Thi 3 5 cac 5 Glr	Phe gag Glu g acc n Thi 235	Arg tgo Cys 220 c ato	Cys 205 c cac His tys Cys	Asp gac Asp cgg	Cys ato Ile tot Ser	Asp cgg Arg ctg Leu 240	Glu cag Gln 225 tcc Ser	Gly 210 ggg Gly	Phe Cor Pro ago Ser	Gln tgo Cys agt	Pro ttt Phe gag Glu 245	Ser gcc 230 gct Ala	Pro 215 gag Glu gto Val	Thr g gto l Val c aco	Leu g ctg L Leu c agg	906 954
99 10: 10: 10: 10: 10: 10:	l acc 2 Thi 3 5 cag 5 Glr 7	Phe gag Glugard Glugar	Arg  g tgo 220 c ato Met 5	Cys 205 c cac s His c tyc t Cys	Asp gac Asp cgg Arg	Cys ato Ile tot Ser	Asp cgg Arg ctg Leu 240	Glu cag Gln 225 ctcc	Gly 210 gggg Gly Gly Ser Ser	Phe ccc Pro	Gln tgc Cys agt Ser	Pro ttt Phe gag Glu 245	Ser  2 gcc 230 gct Ala 3	Pro 215 gag Glu ) gto Val	Thr g gtg val c acc Thi	Leu g ctg L Leu c agg c Arg c gag	906
99 103 103 103 103 103 103 113	1 acc 2 Thi 3 5 cac 6 Glr 7 9 gcc	Phe gag c Glu g acc n Thi 23! c gag a Glu	Arg  g tgo 220 c ato Met 5	Cys 205 c cac s His c tyc t Cys	Asp gac Asp cgg Arg	Cys atcollector tct Ser Gly	Asp cgg Arg ctg Leu 240 ggt	Glu cag Gln 225 ctcc	Gly 210 gggg Gly Gly Ser Ser	Phe ccc Pro	Gln tgo Cys agt Ser tgg	Pro ttt Phe gag Glu 245 ggg	Ser  2 gcc 230 gct Ala 3	Pro 215 gag Glu ) gto Val	Thr g gtg val c acc Thi	Leu g ctg L Leu c agg c Arg c gag s Glu	906 954
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99 103 103 100 100 100 111 111 112 112 123	1 acc 2 Thi 3 5 cas 5 Glr 7 9 gc 0 Ala 1 250 3 ct 4 Leu 5 7 gg 6 Gly 9 1 ctt	Phe gag Glu gacc n Thi 23! c gag a Glu ) c tgt c tca y Sei	Arg  J tgo  220  c ato  Met  J tgo  Cys  t cco  a ggo  r Gly  t cac  a His	Cys 205 C cac S His O tgo t Cys C tgo C tg	Asp gac Sag Cys Cys Cys Cys Cys Thr	Cys atc Ile tct Ser ggg 255 ggt 261 gct Ala	Asp cgg Arg Leu 240 ggt Gly acc Thr	Glu cag Gln 225 tcc Ser Gly Gly ctct Gly Gly Gly Gly Gly	Gly 210 1 999 1 Gly 3 ago 5 ser 2 cgg 7 Arg 2 pr 2 pr 3 pr 4 pr 4 pr 5 pr 6 pr 6 pr 7 pr 7 pr 7 pr 7 pr 8 pr 8 pr 9	Phe coordinates of the coordinat	c agt c agg	Pro ttt pro gag Glu 245 Glu 245 Glu Asp	Ser  E gcc 230 gct Ala 5 g ccc Pro g ctc g ctc c gaa c Glu c ago n Ser	Pro 215 c gag c Glu c gtc c yal c yal c cya c Lett c Let	Thr g gtg acc acc Thr c tgc g Cys c ccc s Pro 280 c cgf s Arc	g ctg Leu c agg c Arg g gag s Glu 265 c cat b His c atg	906 954 1002 1050
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99 103 103 100 100 100 110 111 111 112 122 123 124	1 acc 2 Thi 3 cac 5 Cac 6 Glr 7 gc 0 Ala 1 250 3 ctc 7 gg 8 Gly 1 ctt 2 Leu 3 ttc 6 Phe	Phe gag Glu gacc n Thi 23! c gag a Glu Cys c tca y Sei a Ala	Arg  g tgg g tgg c atg c atg g tgg g tgg t ccc a gg r Gl g tgg t cac a His 300 c tgg g Cys	Cys 205 C cac His Cys C tys C	Asp gac Asp c gac Asp c cgg Arg c tgt Cys Thr G tgt c cys	Cys atc Ile tct Ser ggg Gly 255 ggt Gly Ala	Asp cgg Arg ctg Leu 240 ggt Gly acc Thr gag Cat His	Glu cag Gln 225 tcc Ser Gly Gly tct Gly	Gly 210 1 999 1 Gly 3 ago 2 ser 2 ego 4 Arg 2 y Arg 2 gao 7 Gly 6 tao	Phe ccc responding to the ccc responding to	Gln  tgg  cys  agt  Ser  260  agg  Trr  260  agg  Val	Pro ttt Phe gag Glu 245 Glu 245 Glu Asp Lys ac Asp	Ser  E gcc  E Ala  230  gct  Ala  G ccc  Fro  G ctc  G ago  Sen  310  E gct  Ala  Ala  Ala  Ala  Ala  Ala  Ala  Al	Pro 215 c gag c Glu c gtc c yal c yal c cya c Leu c cya c tya c ty	Thr  g gtg  g acc  acc  Thi  C tgc  C ys  C cc  S Pro  280  C ag  G gg  G gg	Leu g ctg Leu c agg c Arg c gag s Glu 265 c cat his atg Met c tcc	906 954 1002 1050 1098

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165	cta	ggg	ggc	tac	cgc	tgc	agc	tgc	ccc	cag	ggt	ttc	acc	cag	cac	tcc	1674
166	Leu	Gly	Gly	Tyr	Arg	Cys	Ser	Cys	Pro	Gln	Gly	Phe	Thr	Gln	His	Ser	
167		475					480					485				·	
169	cag	tgg	gcc	cag	tgt	gtg	ggt	gag	tgaa	aaag	ggc t	ggga	agaa	ag ct	tgggd	cctc	1728
170	Gln	Trp	Ala	Gln	Cys	Val	Gly	Glu									
	490					495											
												_				gacaa	
			cat o	ctaaa	igati	ig aa	acago	ccac	i cc	cagaa	agat	gaga	atga	igt 9	gtgco	cctgtc	
	gccc				_				٠,								1852
			EQ II														
			ENGTI		97												
			PE:														
						sar	oiens	5									
			EQUE			<b>a</b> 1	3	T	D 1	<b>G</b>		3	77- 7		<b>a</b> 1	G	
		глх	Pro	cys	ьeu	GIN	arg	ьeu	Pro		Ата	Asp	val	Asn	Glu	cys	
187	1.	C1	7 an	Dro	C1	17 n l	Ctra	ШЬъ	N a n	10	370 J	0	37 o 3	3.00	15	7 an	
	HTG	GIU	ASI		етА	val	Cys	THE		стλ	val	Cys	val		Thr	Asp	
190	C1 v	Se.~	Dho	20	Cvc	C1.,	Ctra	Dro	25 Pho	C 17	Птт∽	e~~	T 011	30	Phe	mbr.	
192	сту	Set	35	нта	Cys	GIU	CYS	40	rne	стХ	тЛт	ser.	ьеu 45	ASP	FIIE	THE	
	Glv	Tle		Cvc	V=1	λαν	Thr		Glu	Czzc	Ser	V⇒1		ui ~	Pro	Cvc	
196	GTY	50	MOII	Cys	۷ат	rab	55	voh	GIU	Cys	Set	60	стХ	UTS	FIO	Cys	
100		50					55					30					

RAW SEQUENCE LISTING DATE: 02/21/2002 PATENT APPLICATION: US/09/825,751A TIME: 11:30:33

Input Set : A:\Cura-251.app

Output Set: N:\CRF3\02212002\1825751A.raw

198 199	Gly 65	Gln	Gly	Thr	Cys	Thr 70	Asn	Val	Ile	Gly	Gly 75	Phe	Glu	Cys	Ala	Cys 80
201 202	Ala	Asp	Gly	Phe	Glu 85	Pro	Gly	Leu	Met	Met 90	Thr	Cys	Glu	Asp	Ile 95	Asp
204 205	Glu	Cys	Ser	Leu 100	Asn	Pro	Leu	Leu	Cys 105	Ala	Phe	Arg	Cys	His 110	Asn	Thr
207 208	Glu	Gly	Ser 115	Tyr	Leu	Cys	Thr	Cys 120	Pro	Ala	Gly	Tyr	Thr 125	Leu	Arg	Glu
210 211	Asp	Gly 130	Ala	Met	Cys	Arg	Asp 135	Val	Asp	Glu	Cys	Ala 140	Asp	Gly	Gln	Gln
	Asp 145	Суѕ	His	Ala	Arg	Gly 150	Met	Glu	Cys.	Lys	Asn 155	Leu	Ile	Gly	Thr	Phe 160
217	Ala	-		_	165		_			170					175	
220	Gly	_		180	_			_	185					190		
223	Asn		195					200					205			
226	Glu <sub>.</sub>	210					215					220				
229	Gln 225	_		_		230					235		_			240
232	Ser				245					250					255	
235	Gly			260					265				,	270		
238	Ser		275					280					285			
241		290	_		_		295	_				300				
244	Gly 305		_			310					315					320
247	Gly Cys	_			325					330					335	
250	Gly			340			٠		345					350		
253	Gly		355		-		_	360					365			
256	Cys	370					375					380				
259	385					390					395					400
262	Pro				405					410					415	
265	Cys			420		_		_	425					430		
268			435			_	_	440	_			_	445			
2/0	Ser	ser	GLY	HlS	GTÄ	Cys	GLu	Asp	val	Asn	GLU	cys	Asp	СΤΆ	Pro	HlS

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Input Set : A:\Cura-251.app

Output Set: N:\CRF3\02212002\I825751A.raw

```
450
                            455
271
273 Arg Cys Gln His Gly Cys Gln Asn Gln Leu Gly Gly Tyr Arg Cys Ser
                        470
                                            475
276 Cys Pro Gln Gly Phe Thr Gln His Ser Gln Trp Ala Gln Cys Val Gly
                                        490
279 Glu
284 <210> SEQ ID NO: 3
285 <211> LENGTH: 379
286 <212> TYPE: DNA
287 <213> ORGANISM: Homo sapiens
289 <220> FEATURE:
290 <221> NAME/KEY: CDS
291 <222> LOCATION: (1)..(378)
293 <400> SEQUENCE: 3
294 gga ggg cct gtg att cta ctg cag gca ggc acc ccc cac aac ctc aca
                                                                       48
295 Gly Gly Pro Val Ile Leu Leu Gln Ala Gly Thr Pro His Asn Leu Thr
296
                                         10
                                                                       96
298 tgc cgg gcc ttc aat gcg aag cct gct gcc acc atc atc tgg ttc cgg
299 Cys Arg Ala Phe Asn Ala Lys Pro Ala Ala Thr Ile Ile Trp Phe Arg
                                     25
302 gac ggg acg cag gag ggc gct gtg gcc agc acg gaa ttg ctg aag
                                                                       144
303 Asp Gly Thr Gln Gln Glu Gly Ala Val Ala Ser Thr Glu Leu Leu Lys
304
             35
306 gat ggg aag agg gag acc acc gtg agc caa ctg ctt att aac ccc acg
                                                                       192
307 Asp Gly Lys Arg Glu Thr Thr Val Ser Gln Leu Leu Ile Asn Pro Thr
310 gac ctg gac ata ggg cgt gtc ttc act tgc cga agc atg aac gaa gcc
                                                                       240
311 Asp Leu Asp Ile Gly Arg Val Phe Thr Cys Arg Ser Met Asn Glu Ala
                         70
314 atc cct agt ggc aag gag act tcc atc gag ctg gat gtg cac cac cct
                                                                       288
315 Ile Pro Ser Gly Lys Glu Thr Ser Ile Glu Leu Asp Val His His Pro
                     85
                                          90
318 cct aca gtg acc ctg tcc att gag cca cag acg ggg cag gag ggt gag
                                                                       336
319 Pro Thr Val Thr Leu Ser Ile Glu Pro Gln Thr Gly Gln Glu Gly Glu
                                    105
                100
322 cgt gtt gtc ttt acc tgc cag gcc aca gcc aac ccc gag atc t
                                                                       379
323 Arg Val Val Phe Thr Cys Gln Ala Thr Ala Asn Pro Glu Ile
            115
324
327 <210> SEQ ID NO: 4
328 <211> LENGTH: 126
329 <212> TYPE: PRT
330 <213> ORGANISM: Homo sapiens
332 <400> SEQUENCE: 4
333 Gly Gly Pro Val Ile Leu Leu Gln Ala Gly Thr Pro His Asn Leu Thr
334
                                          10
336 Cys Arg Ala Phe Asn Ala Lys Pro Ala Ala Thr Ile Ile Trp Phe Arg
339 Asp Gly Thr Gln Gln Glu Gly Ala Val Ala Ser Thr Glu Leu Leu Lys
                                 40
```

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 02/21/2002 TIME: 11:30:34

PATENT APPLICATION: US/09/825,751A

Input Set : A:\Cura-251.app

Output Set: N:\CRF3\02212002\I825751A.raw

L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:2236 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 L:2237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 L:2291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61